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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/650,249	08/28/2003	Michael M. Neff	WSHU 2064.1	7302

321 7590 03/24/2006

SENNIGER POWERS
ONE METROPOLITAN SQUARE
16TH FLOOR
ST LOUIS, MO 63102

EXAMINER	
BAUM, STUART F	

ART UNIT	PAPER NUMBER
1638	

DATE MAILED: 03/24/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/650,249	NEFF, MICHAEL M.	
	Examiner	Art Unit	
	Stuart F. Baum	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *07 November 2005*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-88* is/are pending in the application.

4a) Of the above claim(s) *See Continuation Sheet* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *13-21,31,43,46,53,66-71,74 and 76-79* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *28 August 2003* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *4/20/04, 1/21/05*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *sequence search result*.

Continuation of Disposition of Claims: Claims withdrawn from consideration are 1-12,22-30,32-42,44,45,47-52,54-65,72,73,75 and 80-88.

DETAILED ACTION

1. Claims 1-88 are pending.

2. Applicant's election with traverse of Group III, claims 13-21, 31, 32, 46, 53, 66-71, 74, 76-79 and 83, including SEQ ID NO:1 in the reply filed on 11/7/2005 is acknowledged. The traversal is on the ground(s) that Groups VIII-XVI relate to the claims of Group III in that they merely further specify a particular antisense coding nucleotide sequence (page 3 or Remarks, 1st full paragraph). The total number of sequences to be searched would be ten (*Ibid*). Applicants contend that nine additional applications would have to be filed (page 3 of Remarks, 2nd full paragraph). Applicants contend that the MPEP states that up to ten sequences can be included in a single application (page 4 of Remarks, 1st full paragraph).

This is not found persuasive because each sequence requires an independent search of USPTO databases and searching more than one sequence would be an undue burden on USPTO resources. In regards to the permissible number of sequences as specified in the MPEP, those guidelines were for EST sequences which are much shorter than the nucleic acid sequences presented in the present application, and because of the vast number of sequences now present in the current databases that must be searched, the office does not have the resources to search more than one corresponding pair of nucleic acid and amino acid sequences per application. And lastly, according to the MPEP, up to ten sequences will be examined, and one sequence is considered up to ten, for the reasons stated above. In addition, while the search of the prior art for one group may overlap with that of another, they are not co-extensive of each other and thus would be a burden on the Office. Lastly, the Office does not consider financial considerations during the examination process.

The requirement is still deemed proper and is therefore made FINAL.

Claims 1-12, 22-30, 32-42, 44-45, 47-52, 54-65, 72-73, 75, and 80-88 are withdrawn from consideration for being drawn to non-elected inventions.

3. Claims 13-21, 31, 43, 46, 53, 66-71, 74, and 76-79, including SEQ ID NO:1 are examined in the present office action.

Specification

4. The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See for example page 17, line 70. See MPEP § 608.01.

Claim Objections

5. Claim 16 is objected to under 37 CFR 1.75(c), as being of improper dependent form for failing to further limit the subject matter of a previous claim. Applicant is required to cancel the claim(s), or amend the claim(s) to place the claim(s) in proper dependent form, or rewrite the claim(s) in independent form.

Claim 14 is objected to under 37 CFR 1.75(c) as being in improper form because a multiple dependent claim must be stated in the alternative. See MPEP § 608.01(n).

Claim 20 is objected to for stating "any one of". Claim 20 is dependent on one claim.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

6. Claims 13-14, 16-19, 31, 43, 46, 53, 66-67, 69, and 74 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 13-14, 66-67 and 69, are indefinite in the recitation "OBP" or "OBP3". The sole designation of an amino acid sequence by "OBP" or "OBP3" is arbitrary and creates ambiguity in the claims. For example, the amino acid sequence in this application could be designated by some other arbitrary means, or the assignment of said name could be arbitrarily changed to designate a different amino acid sequence. If either event occurs, one's ability to determine the metes and bounds of the claim would be impaired. See *In re Hammack*, 427 F .2d 1378, 1382; 166 USPQ 204, 208 (CCPA 1970). Amendment of the claim to refer to a specific SEQ ID NO would obviate this rejection.

Claim 66 is indefinite in the recitation, "wherein said antisense nucleic acid sequence results in an increase". It is not clear how an antisense nucleic acid sequence can result in anything.

Claim 69 recites the limitation "or plant part" and "the nucleotide sequence in (b)" in claim 66. There is insufficient antecedent basis for this limitation in the claim.

Claims 16, 31, and 74 are indefinite in the recitation "stringent conditions". Applicant does not explicitly disclose specific hybridization conditions that define applicants' recitation of "stringent conditions" (See paragraph 55 bridging pages 12 and 13).

Written Description

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

7. Claims 13-14, 16-21, 31, 43, 46, 53, 66-71, 74, and 76-79 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are drawn to a transgenic plant cell transformed by an OBP antisense coding nucleic acid expression vector, or wherein said OBP is Arabidopsis thaliana OBP3 or orthologs thereof, or wherein the OBP3 coding nucleic acid hybridizes under stringent conditions to SEQ ID NO:1, or plant, or seed produced from said plant; a recombinant antisense expression vector comprising a promoter operable in plant cells and an Arabidopsis thaliana OBP3 antisense coding nucleic acid wherein said OBP3 antisense coding nucleic acid comprises a nucleotide sequence of at least 15 contiguous nucleotides of SEQ ID NO:1, or wherein said nucleic acid hybridizes under a wash stringency equivalent to 0.1X SSC to 2.0X SSC, 0.1% SDS at 50-65^{0}C and which encodes a polypeptide having activity differing from that of Arabidopsis thaliana OBP3 by about 40% or less; a method for producing a transgenic plant having increased size as compared to the corresponding wild-type plant or method for altering the size of the aerial portion of a plant without dwarfing root tissue, comprising transforming plant cells with said recombinant antisense expression vector; a transgenic plant cell transformed by an antisense

nucleic acid sequence complementary to a nucleic acid sequence encoding an OBP3 polypeptide, or wherein said OBP3 is from Arabidopsis thaliana or orthologs thereof, or wherein said nucleic acid sequence hybridizes under a wash stringency equivalent to 0.1X SSC to 2.0X SSC, 0.1% SDS at 50-65^{0}C and which encodes a polypeptide having activity differing from that of Arabidopsis thaliana OBP3 by about 40% or less, or wherein said polypeptide has an activity differing from that of Arabidopsis thaliana OBP3 by about 10%, 20% or 30% or less, or plant, or seed produced from said plant.

Applicants isolated their invention by screening an activation-tagged population of phyB-4 mutants in which Applicants were selecting for suppressors of the phyB-4 mutation phenotype of long hypocotyls (page 62, paragraph 185). Applicants used plasmid rescue techniques to isolate DNA adjacent to the enhancer elements. Applicants disclose the isolated DNA was first called SOB1 which was later changed to OBP3 and includes 1.2kb of non-coding genomic DNA between the enhancer elements and the 3' end of the SOB1/OBP3 ORF and approximately 5.3kb of genomic DNA 5' of the ORF (page 63, Example 3). Applicants do not explicitly define said DNA in terms of SEQ ID NO, but the Office believes this DNA comprises SEQ ID NO:1.

The Applicants do not identify essential regions of the OBP3 protein encoded by SEQ ID NO:1, nor do Applicants describe any polynucleotide sequences that hybridize to SEQ ID NO:1 under stringent conditions or wash conditions as specified for example in claim 68 and which encodes a polypeptide having activity differing from that of Arabidopsis thaliana OBP3 by about 10%, 20%, 30% or 40%.

The Federal Circuit has recently clarified the application of the written description requirement to inventions in the field of biotechnology. See University of California v. Eli Lilly

and Co., 119 F.3d 1559, 1568, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). In summary, the court stated that a written description of an invention requires a precise definition, one that defines the structural features of the chemical genus that distinguishes it from other chemical structures. A definition by function does not suffice to define the genus because it is only an indication of what the gene does, rather than what it is. The court goes on to say, "A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to members of the genus, which features constitute a substantial portion of the genus." *See University of California v. Eli Lilly and Co.*, 119 F.3d 1559; 43 USPQ2d 1398, 1406 (Fed. Cir. 1997).

Applicants fail to describe a representative number of polynucleotide sequences encoding a OBP3 protein falling within the scope of the claimed genus of polynucleotides which hybridize under stringent conditions to SEQ ID NO:1. Applicants only describe a single genomic sequence of SEQ ID NO:1. Furthermore, Applicants fail to describe structural features common to members of the claimed genus of polynucleotides. Hence, Applicants fail to meet either prong of the two-prong test set forth by *Eli Lilly*. Furthermore, given the lack of description of the necessary elements essential for the OBP3 protein, it remains unclear what features identify an Arabidopsis OBP3 protein. Since the genus of OBP3 proteins has not been described by specific structural features, the specification fails to provide an adequate written description to support the breath of the claims.

Enablement

8. Claims 13-21, 31, 43, 46, 53, 66-71, 74, and 76-79 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

The claimed invention is not supported by an enabling disclosure taking into account the *Wands* factors. *In re Wands,* 858/F.2d 731, 8 USPQ2d 1400 (Fed. Cir. 1988). *In re Wands* lists a number of factors for determining whether or not undue experimentation would be required by one skilled in the art to make and/or use the invention. These factors are: the quantity of experimentation necessary, the amount of direction or guidance presented, the presence or absence of working examples of the invention, the nature of the invention, the state of the prior art, the relative skill of those in the art, the predictability or unpredictability of the art, and the breadth of the claim.

The claims are drawn to a transgenic plant cell transformed by an OBP antisense coding nucleic acid expression vector wherein expression of said vector results in an increase in the size of the resulting plant as compared to a corresponding wild-type plant, or wherein said OBP is Arabidopsis thaliana OBP3 or orthologs thereof, or wherein the OBP3 coding nucleic acid hybridizes under stringent conditions to SEQ ID NO:1, or plant, or seed produced from said plant; a recombinant antisense expression vector comprising a promoter operable in plant cells and an Arabidopsis thaliana OBP3 antisense coding nucleic acid wherein said OBP3 antisense coding nucleic acid comprises a nucleotide sequence of at least 15 contiguous nucleotides of SEQ ID NO:1, or wherein said nucleic acid comprises at least 15 contiguous nucleotides and

hybridizes under a wash stringency equivalent to 0.1X SSC to 2.0X SSC, 0.1% SDS at 50-65^{0}C and which encodes a polypeptide having activity differing from that of Arabidopsis thaliana OBP3 by about 40% or less; a method for producing a transgenic plant having increased size as compared to the corresponding wild-type plant or method for altering the size of the aerial portion of a plant without dwarfing root tissue, comprising transforming plant cells with said recombinant antisense expression vector; a transgenic plant cell transformed by an antisense nucleic acid sequence complementary to a nucleic acid sequence encoding an OBP3 polypeptide, or wherein said OBP3 is from Arabidopsis thaliana or orthologs thereof, or wherein said nucleic acid sequence hybridizes under a wash stringency equivalent to 0.1X SSC to 2.0X SSC, 0.1% SDS at 50-65^{0}C and which encodes a polypeptide having activity differing from that of Arabidopsis thaliana OBP3 by about 40% or less, or wherein said polypeptide has an activity differing from that of Arabidopsis thaliana OBP3 by about 10%, 20% or 30% or less, or plant, or seed produced from said plant.

Applicants isolated their invention by screening an activation-tagged population of phyB-4 mutants in which Applicants were selecting for suppressors of the phyB-4 mutation phenotype of long hypocotyls (page 62, paragraph 185). Applicants used plasmid rescue techniques to isolate DNA adjacent to the enhancer elements. Applicants disclose the isolated DNA was first called SOB1 which was later changed to OBP3 and includes 1.2kb of non-coding genomic DNA between the enhancer elements and the 3' end of the SOB1/OBP3 ORF and approximately 5.3kb of genomic DNA 5' of the ORF (page 63, Example 3). Applicants do not explicitly define said DNA in terms of SEQ ID NO, but the Office believes SEQ ID NO:1 comprises said DNA. Applicants disclose that an RNAi construct was created using the 3' end of the coding sequence

which excluded the Dof domain. Arabidopsis plants transformed with said construct exhibited an increase in size compared to wild-type plants (pages 64-66, Example 6).

Because of the indefiniteness of "stringent conditions" as discussed above, the Office interprets this recitation to mean any sequence that hybridizes to SEQ ID NO:1.

Applicants have not reduced the claimed invention to practice. Applicants claims are drawn to either all of SEQ ID NO:1, or any sequence that hybridizes to it. The Office contends that Applicants have not explicitly defined SEQ ID NO:1. As discussed above, Applicants disclose that while cloning the gene responsible for the mutant phenotype, extra 3' and 5' DNA was included. Applicants are silent as to the start and stop codons for the corresponding encoded protein. The Office contends that using DNA that hybridizes to the extra 5' and 3' DNA will not silence an endogenous gene using antisense technology because the 5' and 3' regions are not transcribed. Results from a sequence search of SEQ ID NO:1 indicate that bases 6179-7538 comprise the 35S promoter (sequence search results included). DNA that hybridizes to this region will not produce the expected results when used in antisense technology to down regulate an endogenous gene. In addition, Applicants disclose that they intentionally excluded the nucleic acid segment encoding the Dof domain in their construct. The Office contends that using DNA that hybridizes to this region in antisense technology will produce unexpected results because other genes will be down-regulated that contain the Dof domain but are not responsible for Applicants' claimed phenotype.

The state-of-the-art teaches Dof containing proteins are not all involved in plant size. Papi et al (2002, Plant Physiology 128:411-417; listed in IDS) teach the DAG1 protein, which comprises a Dof domain is involved in light responses and integrity of the testa of Arabidopsis

seeds (abstract). Therefore, using the Dof domain in an antisense construct will downregulate genes not involved in plant stature and will not increase the size of the plant.

Antisense constructs can behave unpredictably when transformed into a heterolgous plant species. Colliver et al (1997, Plant Mol. Biol. 35:509-522) showed that tranformation of bird's foot trefoil with a construct that was antisense to bean chalcone synthase unexpectedly resulted in transformants with *increased* levels of chalcone synthase transcripts (page 519, left column, 2nd paragraph). Emery et al (2003, Current Biology 13:1768-1774) disclose experiments in which a target sequence of a micro-RNA was changed by two base-pairs. The altered base-pairs caused the complementary micro-RNA not to bind to the target sequence, which subsequently led to an increased expression of the target sequence's encoded protein (page 1769, right column, 2nd full paragraph).

The state-of-the-art is such that one of skill in the art cannot predict which nucleic acids that hybrid SEQ ID NO:1 and comprise at least 15 contiguous nucleotides will encode a protein with the same activity as a protein encoded by SEQ ID NO:1. The prediction of protein structure from sequence data and, in turn, utilizing predicted structural determinations to ascertain functional aspects of the protein, is extremely complex, and the positions within the protein's sequence where amino acid substitutions can be made with a reasonable expectation of maintaining function are limited (Bowie et al, Science 247:1306-1310, 1990, see especially page 1306). Proteins may be sensitive to alterations in even a single amino acid in a sequence. For example, the replacement of a glycine residue located within the START domain of either the PHABULOSA or PHAVOLUTA protein receptor with either an alanine or aspartic acid residue,

alters the sterol/lipid binding domain (McConnell et al, Nature 411 (6838):709-713, 2001, see especially page 710, left column, 2nd paragraph).

Applicants have not disclosed how one makes or isolates any of the sequences that are encompassed by Applicants' broad claims. Applicants have not taught which regions of the respective polynucleotides can be used to amplify any of said polynucleotides or which regions can be used as a probe to isolate any of said polynucleotide sequences.

In the absence of guidance, undue trial and error experimentation would be required for one of ordinary skill in the art to screen through the multitude of non-exemplified sequences, either by using non-disclosed fragments of SEQ ID NO:1 as probes or by designing primers to undisclosed regions of SEQ ID NO:1 and isolating or amplifying fragments, subcloning the fragments, producing antisense expression vectors and transforming plants therewith, in order to identify those, if any, that when expressed produce plants exhibiting an increase in size compared to a wild-type plant.

Therefore, given the breadth of the claims; the lack of guidance and examples; the unpredictability in the art; and the state-of-the-art as discussed above, undue experimentation would be required to practice the claimed invention, and therefore the invention is not enabled.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

9. Claims 21 and 71 are rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter.

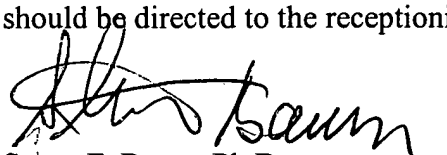
Claims 21 and 71 are drawn to a seed of the transformed plant. Due to Mendelian inheritance of genes, a single gene introduced into a parent plant would only be transferred at most to half the male gametes and half the female gametes. This translates into only three quarters of the progeny having at least a single copy of the transgene and one quarter of the progeny would not carry a copy of the transgene. Given that there is no indication that there would be any other distinguishable characteristics of the claimed seeds, it is unclear whether the claimed seeds would be distinguishable from seeds that would occur in nature. See *Diamond v. Chakrabarty*, 447 U.S. 303 (1980), *Funk Bros. Seed Co. v. Kalo Inoculant Co.*, 333 U.S. 127, 76 USPQ 280 (1948), and *In re Bergy , Coats, and Malik* 195 USPQ 344, (CCPA) 1977. The amendment of the claims to recite that the seeds comprise the construct that was introduced into the parent would overcome the rejection.

10. No claims are allowed.

11. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Stuart F. Baum whose telephone number is 571-272-0792. The examiner can normally be reached on M-F 8:30-5:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Anne Marie Grunberg can be reached at 571-272-0975. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is 571-272-1600.



Stuart F. Baum Ph.D.
Patent Examiner
Art Unit 1638
March 17, 2006

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Qy       6177 TTGTTTCGGATCTAGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCT 6236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      18981 TAGTTTCGGATCTAGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCT 18922

Qy       6237 TCTTTTTCCACGATGTTCCTCGTGGGTGGGGGTCCATCTTTGGGACCACTGTCGGTAGAG 6296
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Qy       6297 GCATCTTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCC 6356
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Qy       6777 AAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACG 6836
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Db      18381 AAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACG 18322

Qy       6837 AGAGTGTCGTGCTCCACCATGTTGGGGATCTAGATATCACATCAATCCACTTGCTTTGAA 6896
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Qy       6897 GACGTGGTTGGAACGTCTTCTTTTTCCACGATGTTCCTCGTGGGTGGGGGTCCATCTTTG 6956
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Qy       6957 GGACCACTGTCGGTAGAGGCATCTTGAACGATAGCCTTTCCTTTATCGCAATGATGGCAT 7016
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Qy       7017 TTGTAGAAGCCATCTTCCTTTTCTACTGTCCTTTCGATGAAGTGACAGATAGCTGGGCAA 7076
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Qy       7077 TGGAATCCGAGGAGGTTTCCCGATATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGG 7136
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Qy       7137 TCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATG 7196
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Db      18021 TCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATG 17962

Qy       7197 TTGGGGATCTAGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCT 7256
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      17961 TTGGGGATCTAGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCT 17902

Qy       7257 TTTTCCACGATGTTCCTCGTGGGTGGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCA 7316
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      17901 TTTTCCACGATGTTCCTCGTGGGTGGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCA 17842

Qy       7317 TCTTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTT 7376
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      17841 TCTTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTT 17782

Qy       7377 TCTACTGTCCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCC 7436
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      17781 TCTACTGTCCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCC 17722

Qy       7437 GATATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTG 7496
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      17721 GATATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTG 17662

Qy       7497 ATATTCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATGTTGGGGATCC 7545
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      17661 ATATTCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATGTTGGGGATCC 17613
```

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RESULT 6
AAA88401/c
ID   AAA88401 standard; DNA; 1361 BP.
XX
AC   AAA88401;
XX
DT   09-JAN-2001  (first entry)
XX
DE   4X CaMV 35S enhancer construct.
XX
KW   CaMV; 35S; enhancer; trait-associated gene identification;
KW   activation tagging; fruit; transgenic plant; ss.
XX
OS   Cauliflower mosaic virus.
XX
FH   Key             Location/Qualifiers
FT   repeat_region   1. .1354
FT                   /*tag=  a
FT                   /repeat_type= TANDEM
FT                   /note= "4 CaMV 35S enhancer units"
FT   repeat_unit     1. .339
FT                   /*tag=  b
FT                   /note= "CaMV 35S enhancer unit 1"
FT   enhancer        1. .129
FT                   /*tag=  c
FT                   /note= "CaMV 35S enhancer AluI-EcoRV fragment"
FT   enhancer        130. .331
FT                   /*tag=  d
FT                   /note= "129 bp fragment of the CaMV sequence"
FT   enhancer        333. .339
FT                   /*tag=  e
FT                   /note= "additional 7 bp not associated with 35S enhancer"
FT   repeat_unit     340. .678
FT                   /*tag=  f
FT                   /note= "CaMV 35S enhancer unit 2"
FT   enhancer        340. .541
FT                   /*tag=  g
FT                   /note= "CaMV 35S enhancer AluI-EcoRV fragment"
FT   enhancer        542. .670
FT                   /*tag=  h
FT                   /note= "129 bp fragment of the CaMV sequence"
FT   enhancer        672. .678
FT                   /*tag=  i
FT                   /note= "additional 7 bp not associated with 35S enhancer"
FT   repeat_unit     679. .1017
FT                   /*tag=  j
FT                   /note= "CaMV 35S enhancer unit 3"
FT   enhancer        679. .880
FT                   /*tag=  k
FT                   /note= "CaMV 35S enhancer AluI-EcoRV fragment"
FT   enhancer        881. .1009
FT                   /*tag=  l
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FT                   /note= "129 bp fragment of the CaMV sequence"
FT   enhancer        1011. .1017
FT                   /*tag=  m
FT                   /note= "additional 7 bp not associated with 35S enhancer"
FT   repeat_unit     1018. .1354
FT                   /*tag=  a
FT                   /note= "CaMV 35S enhancer unit 4"
FT   enhancer        1018. .1219
FT                   /*tag=  n
FT                   /note= "CaMV 35S enhancer AluI-EcoRV fragment"
FT   enhancer        1220. .1348
FT                   /*tag=  o
FT                   /note= "129 bp fragment of the CaMV sequence"
FT   enhancer        1350. .1354
FT                   /*tag=  p
FT                   /note= "additional 6 bp not associated with 35S enhancer"
XX
PN   WO200053794-A2.
XX
PD   14-SEP-2000.
XX
PF   09-MAR-2000; 2000WO-US006298.
XX
PR   12-MAR-1999;   99US-0124232P.
XX
PA   (AGRI-) AGRITOPE INC.
XX
PI   Wagner R,  Mathews H,  Liu XL,  Waggoner WJ;
XX
DR   WPI; 2000-594336/56.
XX
PT   Identifying genes associated with a desired trait for isolating and
PT   characterizing the genes comprises using an enhancer element which
PT   enhances gene expression and stably integrates into the plant genome.
XX
PS   Claim 4; Fig 5; 42pp; English.
XX
CC   The present sequence is that of a 4X cauliflower mosaic virus (CaMV) 35S
CC   enhancer sequence preferred for use in the method of the invention. It
CC   includes 4 repeats of 202 bp AluI-EcoRV fragments of the 35S enhancer,
CC   129 bp of the CaMV sequence associated with each tandem Alu-EcoRV repeat,
CC   and an additional 7 bp repeated sequence, which does not appear in the
CC   35S enhancer region of the native CaMV genome. This 4X CaMV 35S enhancer
CC   element can be used in a method for identifying genes associated with a
CC   desired trait in a fruit-bearing plant. The method involves: transforming
CC   plant cells with an activation tagging vector comprising an element which
CC   functions to enhance gene expression and has the ability to integrate
CC   into the plant genome in a manner effective to enhance expression of
CC   native plant genes, selecting transformed plant cells, regenerating
CC   transformed plant cells to yield mature plants, selecting plants having a
CC   desired trait, identifying, isolating and characterizing genes the
CC   transcription of which has been enhanced, and confirming the contribution
CC   of the modified expression of each identified gene to the desired trait.
CC   The desired trait may be increased resistance to fungal, bacterial or
CC   viral pathogens, insects, modifications in flower size, flower number,
CC   flower pigmentation and shape, modified leaf number, leaf pigmentation
CC   and shape, modified seed number, pattern or distribution of leaves and
CC   flowers, modified stem length between nodes, root mass or root
CC   development characteristics or increased drought, salt and antibiotic
CC   tolerance. Plants having short life cycles are transformed, as
CC   exemplified by dwarf varieties of tomato
XX
SQ   Sequence 1361 BP; 447 A; 332 C; 297 G; 285 T; 0 U; 0 Other;

  Query Match             17.9%;  Score 1360;  DB 3;  Length 1361;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-201;
  Matches 1360;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6179 GTTTCGGATCTAGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTC 6238
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1360 GTTTCGGATCTAGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTC 1301

Qy       6239 TTTTTCCACGATGTTCCTCGTGGGTGGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGC 6298
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1300 TTTTTCCACGATGTTCCTCGTGGGTGGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGC 1241

Qy       6299 ATCTTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTT 6358
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1240 ATCTTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTT 1181

Qy       6359 TTCTACTGTCCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCC 6418
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1180 TTCTACTGTCCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCC 1121

Qy       6419 CGATATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTT 6478
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1120 CGATATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTT 1061

Qy       6479 GATATTCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATGTTGGGGATCTAGATATCACA 6538
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1060 GATATTCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATGTTGGGGATCTAGATATCACA 1001

Qy       6539 TCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTTTTTCCACGATGTTCCTCGT 6598
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1000 TCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTTTTTCCACGATGTTCCTCGT 941

Qy       6599 GGGTGGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGATAGCCTTTCC 6658
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        940 GGGTGGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGATAGCCTTTCC 881

Qy       6659 TTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTTCTACTGTCCTTTCGATGAA 6718
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 TTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTTCTACTGTCCTTTCGATGAA 821

Qy       6719 GTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCCTTTGTTGAAA 6778
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        820 GTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCCTTTGTTGAAA 761

Qy       6779 AGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAG 6838
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 AGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAG 701

Qy       6839 AGTGTCGTGCTCCACCATGTTGGGGATCTAGATATCACATCAATCCACTTGCTTTGAAGA 6898
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 AGTGTCGTGCTCCACCATGTTGGGGATCTAGATATCACATCAATCCACTTGCTTTGAAGA 641

Qy       6899 CGTGGTTGGAACGTCTTCTTTTTCCACGATGTTCCTCGTGGGTGGGGGTCCATCTTTGGG 6958
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        640 CGTGGTTGGAACGTCTTCTTTTTCCACGATGTTCCTCGTGGGTGGGGGTCCATCTTTGGG 581

Qy       6959 ACCACTGTCGGTAGAGGCATCTTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTT 7018
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 ACCACTGTCGGTAGAGGCATCTTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTT 521

Qy       7019 GTAGAAGCCATCTTCCTTTTCTACTGTCCTTTCGATGAAGTGACAGATAGCTGGGCAATG 7078
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 GTAGAAGCCATCTTCCTTTTCTACTGTCCTTTCGATGAAGTGACAGATAGCTGGGCAATG 461

Qy       7079 GAATCCGAGGAGGTTTCCCGATATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTC 7138
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 GAATCCGAGGAGGTTTCCCGATATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTC 401

Qy       7139 TTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATGTT 7198
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 TTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATGTT 341

Qy       7199 GGGGATCTAGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTT 7258
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 GGGGATCTAGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTT 281

Qy       7259 TTCCACGATGTTCCTCGTGGGTGGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATC 7318
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 TTCCACGATGTTCCTCGTGGGTGGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATC 221

Qy       7319 TTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTTC 7378
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        220 TTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTTC 161

Qy       7379 TACTGTCCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGA 7438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 TACTGTCCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGA 101

Qy       7439 TATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGAT 7498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 TATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGAT 41

Qy       7499 ATTCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATGTTG 7538
              |||||||||||||||||||||||||||||||||||||||
Db          40 ATTCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATGTTG 1
```

RESULT 7
ADL71845
ID ADL71845 standard; DNA; 1235 BP.
XX
AC ADL71845;
XX
DT 20-MAY-2004 (first entry)
XX
DE Arabidopsis thaliana OBP3 antisense DNA #6.
XX
KW Transgenic plant; Dof transcription factor; ocs binding factor;
KW plant size; plant stature; root growth; plant; gene; ds; OBF;
KW OBF binding protein; OBP3; SOB1; mouse-ear cress.
XX
OS Arabidopsis thaliana.
XX
PN US2004045055-A1.
XX
PD 04-MAR-2004.
XX
PF 28-AUG-2003; 2003US-00650249.
XX
PR 28-AUG-2002; 2002US-0406657P.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Neff MM;
XX
DR WPI; 2004-225757/21.
XX
PT New transgenic plant cell, useful in producing plants with altered size
PT and stature and with normal and healthy root growth.
XX
PS Claim 37; SEQ ID NO 17; 53pp; English.
XX
CC The invention relates to a transgenic plant transformed by a Dof
CC transcription factor, OBF (ocs binding factor) binding protein (OBP3).
CC OBP3 is also known as SOB1. The transgenic plant cell and OBP3 nucleic
CC acid and polypeptides are useful in producing transgenic plants with
CC altered size and stature and with normal and healthy root growth. The
CC present sequence is Arabidopsis thaliana OBP3 antisense DNA.
XX
SQ Sequence 1235 BP; 408 A; 222 C; 179 G; 426 T; 0 U; 0 Other;

  Query Match   16.3%; Score 1235; DB 12; Length 1235;
  Best Local Similarity 100.0%; Pred. No. 9e-182;
  Matches 1235; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy       3045 CAACCAAGAACGATGACGTATATGATTGACTTGCAAAAATAAGCAAACAAAATACCTGTT 3104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAACCAAGAACGATGACGTATATGATTGACTTGCAAAAATAAGCAAACAAAATACCTGTT 60

Qy       3105 CAAATCGACACTTAATTCCAAAAAGGTTAGTAATAAGTAAGAAGGCTTTTATTTATGAAA 3164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAAATCGACACTTAATTCCAAAAAGGTTAGTAATAAGTAAGAAGGCTTTTATTTATGAAA 120

Qy       3165 ACAAAAAGAAATAAAGAGCCTAAGAGAATGATGAAAATTGAAAGAGAAAAAAGAGCATTG 3224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAAAAAGAAATAAAGAGCCTAAGAGAATGATGAAAATTGAAAGAGAAAAAAGAGCATTG 180

Qy       3225 TTATAGAAAAGAAAAAAAAAGAGAGAGTAAAGAGAATTAAGAAACACAATAAATTAAACAA 3284
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTATAGAAAAGAAAAAAAAAGAGAGAGTAAAGAGAATTAAGAAACACAATAAATTAAACAA 240

Qy       3285 AGGAAACTTCATTTCTTCTCTTTATCCCATTCAGCTCCTCCCTTCTCTCTCTCTCTCTCT 3344
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGAAACTTCATTTCTTCTCTTTATCCCATTCAGCTCCTCCCTTCTCTCTCTCTCTCTCT 300

Qy       3345 CTCTCTCTCTCTAGATCAATTCTTTCTTCTATGATGTGATTATCCACCATATCTGCGACC 3404
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCTCTCTCTCTAGATCAATTCTTTCTTCTATGATGTGATTATCCACCATATCTGCGACC 360

Qy       3405 TCTTACCTAAAAAGGATACAAGTAAGAGATTCAAAGATGGTTTTCTCATCTCTTCCAGTG 3464
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Db        361 TCTTACCTAAAAAGGATACAAGTAAGAGATTCAAAGATGGTTTTCTCATCTCTTCCAGTG 420

Qy       3465 AATCAGTTCGATTCCCAAAATTGGCAGCAGGTAAAAATCAGTTTATGATATTTGCTAGAT 3524
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AATCAGTTCGATTCCCAAAATTGGCAGCAGGTAAAAATCAGTTTATGATATTTGCTAGAT 480

Qy       3525 GTTTCTGATTCGTTCCTTTTTCCTCCAAGCTCGATCAAGATTTATGAAAATTTGATGAGA 3584
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTTTCTGATTCGTTCCTTTTTCCTCCAAGCTCGATCAAGATTTATGAAAATTTGATGAGA 540

Qy       3585 TTTTGTTCGACAAAATTCCTAGCTATTGTGGACGCGCATATATATTACTTATGAATATTC 3644
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTTGTTCGACAAAATTCCTAGCTATTGTGGACGCGCATATATATTACTTATGAATATTC 600

Qy       3645 TTAGTTGATTAAACCCTTTTTTTTTCTTGTCTTCTCGAATATACGAAAATATATAAAGAT 3704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTAGTTGATTAAACCCTTTTTTTTTCTTGTCTTCTCGAATATACGAAAATATATAAAGAT 660

Qy       3705 GATTTCAATTTTGGTCTTTTTTTCTACTTCAAGACTTTTTAAAAAATTATTCTTAGTTGA 3764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GATTTCAATTTTGGTCTTTTTTTCTACTTCAAGACTTTTTAAAAAATTATTCTTAGTTGA 720

Qy       3765 TAAAAACCTTTTTTTCTTGTCTTCTCCAAGGGCTTATGTATAATGTTTTTCTTACAGGATT 3824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TAAAAACCTTTTTTTCTTGTCTTCTCCAAGGGCTTATGTATAATGTTTTTCTTACAGGATT 780

Qy       3825 AATTTTCTCTTTGGTTAGATTTTTACACCGCCATGGAATTATCACTTCAAAAATAAAAAA 3884
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AATTTTCTCTTTGGTTAGATTTTTACACCGCCATGGAATTATCACTTCAAAAATAAAAAA 840

Qy       3885 GTTTAAAGTTACTATGACTTTAATCTGAGTTATTTATCCATTTTCTTTTTGCAGCTTTGT 3944
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GTTTAAAGTTACTATGACTTTAATCTGAGTTATTTATCCATTTTCTTTTTGCAGCTTTGT 900

Qy       3945 TGAAAAACTATAATTAATCTGCAATTCTTGTCAAAGTAGTCACAATTTTTATCTATTTTC 4004
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGAAAAACTATAATTAATCTGCAATTCTTGTCAAAGTAGTCACAATTTTTATCTATTTTC 960

Qy       4005 TTTTGTCTCCGACCAATGTTTCAAACTCGAATCCTTTCGTTAAAAGTTGTTTCTGCTTTA 4064
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTTTGTCTCCGACCAATGTTTCAAACTCGAATCCTTTCGTTAAAAGTTGTTTCTGCTTTA 1020

Qy       4065 TTATAAACCTGAAACTAATTAGTACAAATTATGTTAATATGCAGCAAGGGAACCAACATC 4124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTATAAACCTGAAACTAATTAGTACAAATTATGTTAATATGCAGCAAGGGAACCAACATC 1080

Qy       4125 AGCTAGAATGTGTCACAACTGACCAGAACCCTAATAATTACTTACGGCAGCTCTCATCAC 4184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGCTAGAATGTGTCACAACTGACCAGAACCCTAATAATTACTTACGGCAGCTCTCATCAC 1140

Qy       4185 CACCGACTTCTCAGGTTGCAGGTTCGAGTCAAGCTAGAGTGAATTCAATGGTGGAACGTG 4244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CACCGACTTCTCAGGTTGCAGGTTCGAGTCAAGCTAGAGTGAATTCAATGGTGGAACGTG 1200

Qy       4245 CTCGGATCGCAAAAGTCCCATTGCCTGAAGCAGCT 4279
              |||||||||||||||||||||||||||||||||||
Db       1201 CTCGGATCGCAAAAGTCCCATTGCCTGAAGCAGCT 1235
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